

Figure 1 (SEQ ID NO:724)

85P1B3 SSH sequence and GenBank homology to OIP5

GATCAGAGGACACATGGGACTCTGCATCTTAATTCTAAATITACAGTCAAAGACATTTCAAG
AGATAAGTATTATGAATTCAATAAGAACTAAAGTAAGTCTTAAGGCAAATAGCTATAAAA
GAGAAGAACCTTCTAGTCTCATCTTCTAAAAACAGCTCACAAATAATTGGAAAATCAGCC
TAAAGGTAAATAGAAACTGCATTCCCCTCCATTCTGAAGGCCAATCTTTCAAGAAATGAC
TAAGCAGCACCTGTTGAAGACAGCAATAAGCCTGAACCTGACACTCAAGCTTGGTACA
GGATC

gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein... 632 e-179
gb|AF158642.1|AF158642 Homo sapiens metalloproteinase-disin... 42 0.12
gb|AC005075.2|AC005075 Homo sapiens clone RG219E16, complet... 42 0.12
emb|AL096773.6|HS1000E10 Human DNA sequence from clone 1000... 40 0.48

>gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein OIP5 mRNA, partial cds
Length = 1197

Score = 632 bits (319), Expect = e-179

Identities = 319/319 (100%)

Strand = Plus / Minus

Query: 1 gatcagaggacacatggactctgcatcttaattcctaaatttacagtcaaagacat 60
||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 1013 gatcagaggacacatggactctgcatcttaattcctaaatttacagtcaaagacat 954

Query: 61 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatacgta 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 953 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatacgta 894

Query: 121 taaaagagaagaatccttagtctctatcttctaaaaacagcttcacaaataattggaa 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 893 taaaagagaagaatccttagtctctatcttctaaaaacagcttcacaaataattggaa 834

Query: 181 aatcagcctaaaggtaaatagaaactgcatttccccccattcttgaagccaatctttt 240
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 833 aatcagcctaaaggtaaatagaaactgcatttccccccattcttgaagccaatctttt 774

Query: 241 caagaatgactaaggcacctgttgaagacagcaataaagcctgaacctgacact 300
|||||||
Sbjct: 773 caagaatgactaaggcacctgttgaagacagcaataaagcctgaacctgacact 714

Figure 2

cDNA Sequence and ORF of 85P1B3/OIPS clone A
(SEQ ID NO:727)

5' → 9 18 27 36 45 54
 5' GGC TGC GGG AAG ATG GCG GCT CAG CCG CTG CGG CAT CGC TCA CGT TGT GCA ACG
 (SEQ ID NO:728) → M A A Q P L R H R S R C A T
 63 72 81 90 99 108
 CCG CCC CGG GGG GAC TTT TGT GGT GGC ACT GAG AGG GCG ATT GAC CAA GCT TCT
 P P R G D F C G G T E R A I D Q A S
 117 126 135 144 153 162
 TTT ACG ACC TCC ATG GAG TGG GAT ACG CAG GTG GTG AAG CGG TCC TCG CCG CTC
 F T T S M E W D T Q V V K G S S P L
 171 180 189 198 207 216
 GGC CCC GCA GGG CTG GGG GCT GAG GAG CCA GCC GCC GGC CCG CAG CTG CCG TCT
 G P A G L G A E E P A A G P Q L P S
 225 234 243 252 261 270
 TGG CTG CAG CCT GAG AGG TGC GCT GTG TTC CAG TGC GCA CAG TGT CAC GCA GTG
 W L Q P E R C A V F Q C A Q C H A V
 279 288 297 306 315 324
 CTC GCC GAC TCG GTG CAC CTC GCC TGG GAC CTG TCG CGG TCC CTC GGG GCC GTG
 L A D S V H L A W D L S R S L G A V
 333 342 351 360 369 378
 GTC TTC TCC AGA GTT ACA AAT AAC GTC GTT TTG GAA GCG CCC TTC CTA GTT GGC
 V F S R V T N N V V L E A P F L V G
 387 396 405 414 423 432
 ATT GAA GGT TCA CTC AAA GGC AGT ACT TAC AAC CTT TTA TTC TGT GGT TCT TGT
 I E G S L K G S T Y N L L F C G S C
 441 450 459 468 477 486
 GGG ATT CCC GTT GGT TTC CAT CTG TAT TCT ACC CAT GCT GGC CTG GCT GCC TTG
 G I P V G F H L Y S T H A A L A A L
 495 504 513 522 531 540
 AGA GGT CAC TTC TGC CTT TCC AGT GAC AAA ATG GTG TGC TAT CTC TTA AAA ACA
 R G H F C L S S D K M V C Y L L K T
 549 558 567 576 585 594
 AAA GCC ATA GTC ATT GCA TCA GAG ATG GAT ATT CAA AAT GTT CCT CTA TCA GAA
 K A I V N A S E M D I Q N V P L S E
 603 612 621 630 639 648
 AAG ATT GCA GAG CTG AAA GAG AAG ATA GTG CTA ACG CAC AAT CGC TTA AAA TCA
 K I A E L K E K I V L T H N R L K S

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Figure 3

85P1B3/OIP5 protein sequence. (SEQ ID NO:729)

1 MAAQPLRHRs RCATPPRGDF CGGTERAIDQ ASFTTSMEDW TQVVKGSSPL GPAGLGAEFP
61 AAGPQLPSWL QPERCAVFQC AQCCHAVALADS VHLAWDLSRS LGAVVFSRVT NNVVLEAPFL
121 VGIEGSLKGS TYNLLFCGSC GIPVGFHLYS THAALAALRG HFCLSSDKMV CYLLKTKAIV
181 NASEMDIQNV PLSEKIAELK EKIVLTHNRL KSLMKILSEV TPDQSKPEN*

Figure 4

Alignment of 85P1B3 with OIP5.

>gi|2815610|gb|AAC39561.1| (AF025441) Opa-interacting protein OIP5 [Homo sapiens]
Length = 231

Score = 462 bits (1189), Expect = e-130

Identities = 229/229 (100%), Positives = 229/229 (100%)

85P1B3: 1	MAAQPLRHSRCATPPRGDFCGGTERAIDQASFTTSM	MEWDTQVVKGSSPLGPAGLGAEEP	60		
	MAAQPLRHSRCATPPRGDFCGGTERAIDQASFTTSM	MEWDTQVVKGSSPLGPAGLGAEEP			
OIP5: 3	MAAQPLRHSRCATPPRGDFCGGTERAIDQASFTTSM	MEWDTQVVKGSSPLGPAGLGAEEP	62		
85P1B3: 61	AAGPQLPSWLQPERCAVFQCAQCHA	VLDSTVHLAWDLSRS	LGAVVFSRV	TNNVLEAPFL	120
	AAGPQLPSWLQPERCAVFQCAQCHA	VLDSTVHLAWDLSRS	LGAVVFSRV	TNNVLEAPFL	
OIP5: 63	AAGPQLPSWLQPERCAVFQCAQCHA	VLDSTVHLAWDLSRS	LGAVVFSRV	TNNVLEAPFL	122
85P1B3: 121	VGIEGSLKGSTYNNLFCGSCGIPVGFHLYST	HAALAALRGHFC	LSSDKMVCYLLKTAIV	180	
	VGIEGSLKGSTYNNLFCGSCGIPVGFHLYST	HAALAALRGHFC	LSSDKMVCYLLKTAIV		
OIP5: 123	VGIEGSLKGSTYNNLFCGSCGIPVGFHLYST	HAALAALRGHFC	LSSDKMVCYLLKTAIV	182	
85P1B3: 181	NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLM	KILSEVTPDQSKPEN	229 (SEQ ID NO:730)		
	NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLM	KILSEVTPDQSKPEN			
OIP5: 183	NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLM	KILSEVTPDQSKPEN	231 (SEQ ID NO:731)		

Fig. 21A

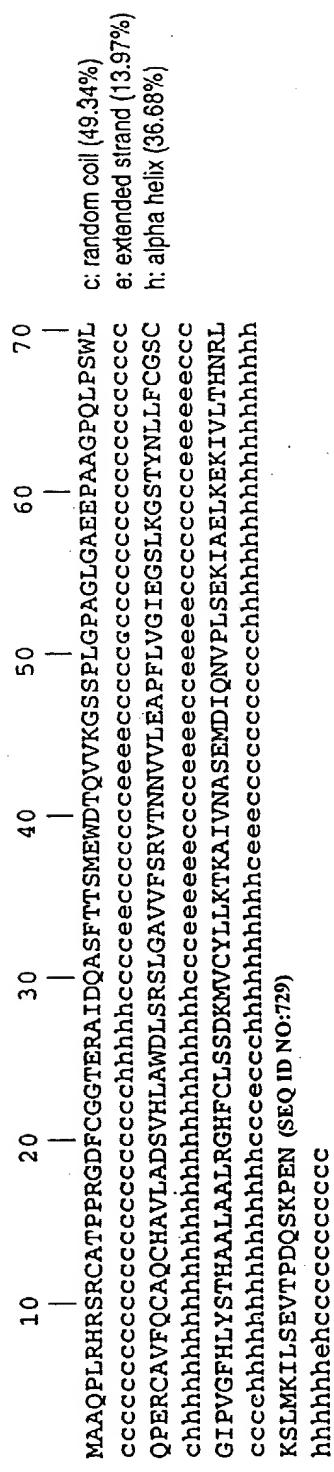


Fig. 21B

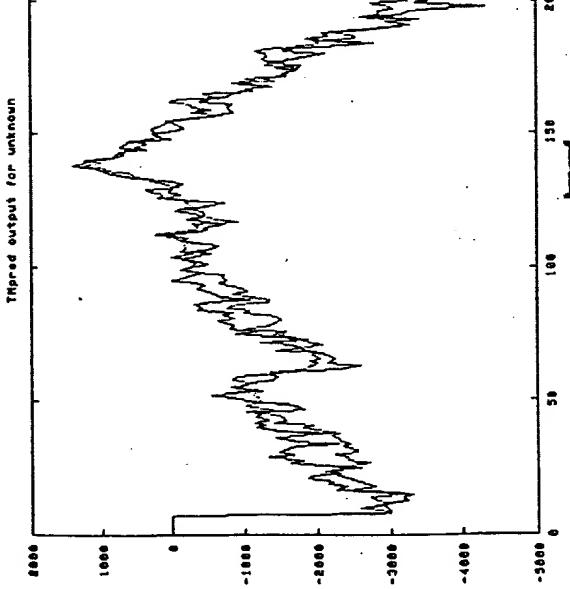
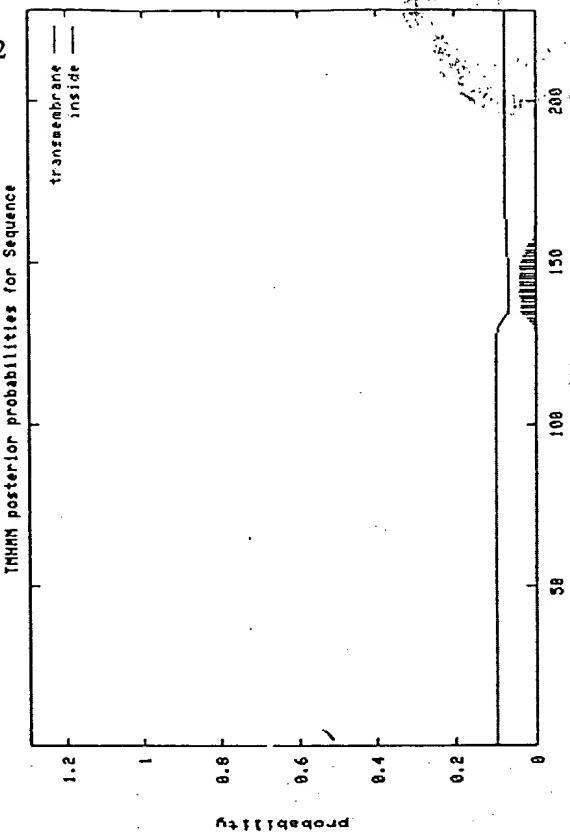


Fig. 21C



1 transmembrane from amino acids 129-149